



# SEQUENCE LISTING

<110> Gurney, Mark E.

Li, Jinhe

Pauley, Adele M.

Pharmacia & Upjohn Company

<120> Human Sel-10 Polypeptides and Polynucleotides that  
Encode Them

<130> 6142

<140> 6142

<141> 1997-12-19

<160> 32

<170> PatentIn Ver. 2.0

<210> 1

<211> 3550

<212> DNA

<213> Homo sapiens

<220>

<221> misc\_feature

<222> (2485)..(2485)

<223> residue uncertain

<220>

<221> misc\_feature

<222> (3372)..(3372)

<223> residue uncertain

<400> 1

ctcattatttc cctcgagttc ttctcagtc a gctgcatgt atgtatgtgt gtcccgagaa 60

gcggtttgat actgagctgc atttgcc ttt actgtggagt tttgttgccg gttctgctcc 120

ctaattcttcc tttttctgacg tgccctgagca tgtccacatt agaattctgtg acatacctac	180
ctgaaaaagg ttttatattgt cagagactgc caagcagccg gacacacggg ggcacagaat	240
cactgaaggg gaaaaataca gaaaatatgg gtttctacgg cacattaata atgatttttt	300
acaaaatgaa aagaaagtgt gaccatgggt ctgagggtccg ctctttttct ttgggaaaga	360
aaccatgcaa agtctcagaa tatacaagta ccactgggct tgtaccatgt tcagcaacac	420
caacaacttt tggggacctc agagcagcca atggccaagg gcaacaacga cgccgaatta	480
catctgtcca gccacctaca ggccctcagg aatggctaaa aatgtttcag agctggagtgt	540
gaccagagaa attgcttgct ttagatgaac tcattgatag ttgtgaacca acacaagtaa	600
aacatatgat gcaagtgata gaaccccagt ttcaacgaga cttcatttca ttgctcccta	660
aagagttggc actctatgtg ctttcattcc tgggaaccaa agacctgcta caagcagctc	720
agacatgtcg ctactggaga attttggctg aagacaacct tctctggaga gagaaatgca	780
aagaagaggg gattgatgaa ccattgcaca tcaagagaag aaaagtaata aaaccaggtt	840
tcatacacag tccatggaaa agtgcataca tcagacagca cagaattgat actaactgga	900
ggcgaggaga actcaaactc cctaagggtgc tgaaaggaca tgatgatcat gtgatcacat	960
gcttacagtt ttgtggtaac cgaatagtta gtgggttctga tgacaacact ttaaaagttt	1020
ggtcagcagt cacaggcaaa tgtctgagaa cattagtggg acatacaggt ggagtatggt	1080
catcacaaat gagagacaac atcatcatta gtggatctac agatcggaca ctcaaagtgt	1140
ggaatgcaga gactggagaa tgtatacaca ccttatatgg gcatacttcc actgtgcgtt	1200
gtatgcatct tcatgaaaaa agagttgtta gcgggttctcg agatgccact cttagggttt	1260
gggatattga gacaggccag tgtttacatg ttttgatggg tcatgttgca gcagtccgct	1320
gtgttcaata tgatggcagg agggttgtta gtggagcata tgattttatg gtaaagggtgt	1380
gggatccaga gactgaaacc tgtctacaca cgttgcaggg gcataactaat agagtctatt	1440
cattacagtt tgatggtatc catgtggtga gtggatctct tgatacatca atccgtgttt	1500
gggatgtgga gacagggaat tgcattcaca cgttaacagg gcaccagtcg ttaacaagtg	1560
gaatggaact caaagacaat attcttgtct ctgggaatgc agattctaca gttaaaactc	1620
gggatatcaa aacaggacag tgtttacaaa cattgcaagg tcccaacaag catcagagtgt	1680
ctgtgacctg tttacagttc aacaagaact ttgtaattac cagctcagat gatggaactg	1740
taaaactatg ggacttgaaa acgggtgaat ttattcgaaa cctagtcaca ttggagagtgt	1800
gggggagtgg gggagttgtg tggcggtatca gagcctcaaa cacaagctg gtgtgtgcag	1860

ttgggagtcg gaatgggact gaagaaacca agctgctggt gctggacttt gatgtggaca	1920
tgaagtgaag agcagaaaag atgaatttgt ccaatttgtt agacgatata ctccctgccc	1980
ttccccctgc aaaaagaaaa aaagaaaaga aaaagaaaaa aatcccttgt tctcagtggg	2040
gcaggatggt ggcttggggc aacagattga aaagacctac agactaagaa ggaaaagaag	2100
aagagatgac aaaccataac tgacaagaga ggcgtctgct gtctcatcac ataaaaggct	2160
tcacttttga ctgagggcag ctttgcaaaa tgagactttc taaatcaaac caggtgcaat	2220
tatttcttta ttttcttctc cagtgggtcat tggggcagtg ttaatgctga aacatcatta	2280
cagattctgc tagcctgttc ttttaccact gacagctaga cacctagaaa ggaactgcaa	2340
taatatacaa acaagtactg gttgactttc taattagaga gcatctgcaa caaaaagtca	2400
tttttctgga gtggaaaagc ttaaaaaaat tactgtgaat tgtttttgta cagttatcat	2460
gaaaagcttt tttttttatt ttttngccaa ccattgccaa tgtcaatcaa tcacagtatt	2520
agcctctggt aatctattta ctgttgcttc catatacatt cttcaatgca tatgttgctc	2580
aaagggtggc agttgtcctg ggttctgtga gtcctgagat ggatttaatt cttgatgctg	2640
gtgctagaag taggtcttca aatatgggat tgttgctcca accctgtact gtactcccag	2700
tggccaaact tatttatgct gctaaatgaa agaaagaaaa aagcaaatta ttttttttat	2760
tttttttctg ctgtgacgtt ttagtcccag actgaattcc aaatttgctc tagtttggtt	2820
atggaaaaaa gactttttgc cactgaaact tgagccatct gtgcctctaa gaggctgaga	2880
atggaagagt ttcagataat aaagagtga gtttgctgctc aagtaaagaa ttgagagtgt	2940
gtgcaaagct tattttcttt tatctgggca aaaattaaaa cacattcctt ggaacagagc	3000
tattacttgc ctgttctgtg gagaaacttt tctttttgag ggctgtggtg aatggatgaa	3060
cgtacatcgt aaaactgaca aaatatattta aaaatatata aaacacaaaa ttaaaataaa	3120
gttgctgggc agtcttagtg ttttacagta tttgggaaaa caactgttac agttttattg	3180
ctctgagtaa ctgacaaagc agaaactatt cagtttttgt agtaaaggcg tcacatgcaa	3240
acaaacaaaa tgaatgaaac agtcaaatgg tttgcctcat tctccaagag ccacaactca	3300
agctgaactg tgaaagtggg ttaacactgt atcctaggcg atcttttttc ctcttctgt	3360
ttattttttt gnttgtttta tttatagtct gatttaaaac aatcagattc aagttgggta	3420
attttagtta tgtaacaacc tgacatgatg gagggaaaaca accttaaaag ggattgtgct	3480
tatggtttga ttcacttaga aattttattt tcttataact taagtgaat aaaatgtggt	3540

ttttcatggt

3550

<210> 2  
<211> 3571  
<212> DNA  
<213> Homo sapiens

<220>  
<221> misc\_feature  
<222> (2506)..(2506)  
<223> residue uncertain

<220>  
<221> misc\_feature  
<222> (3393)..(3393)  
<223> residue uncertain

<400> 2  
ctcagcaggt caggacattt ggtaggggaa ggttgaaaga caaaagcagc aggccttggg 60  
ttctcagcct tttaaaaact attattaaat atatattttt aaaatttagt ggtagagct 120  
tttagtaatg tgctgtatt acatgtagag agtattcgtc aaccaagagg agttttaaaa 180  
tgtcaaaacc gggaaaacct actctaaacc atggcttggg tctgttgat cttaaaagtg 240  
caaaagagcc tctaccacat caaacctga tgaagatatt tagcattagc atcattgccc 300  
aaggcctccc tttttgtcga agacggatga aaagaaagt ggaccatggg tctgaggtcc 360  
gctctttttc tttgggaaag aaaccatgca aagtctcaga atatacaagt accactgggc 420  
ttgtaccatg ttcagcaaca ccaacaactt ttggggacct cagagcagcc aatggccaag 480  
ggcaacaacg acgccgaatt acatctgtcc agccacctac aggcctccag gaatggctaa 540  
aaatgtttca gagctggagt ggaccagaga aattgcttgc ttagatgaa ctcatgata 600  
gttgtgaacc aacacaagta aaacatatga tgcaagtgat agaaccacag tttcaacgag 660  
acttcatttc attgctccct aaagagttgg cactctatgt gctttcatte ctggaacca 720  
aagacctgct acaagcagct cagacatgtc gctactggag aattttggct gaagacaacc 780  
ttctctggag agagaaatgc aaagaagagg ggattgatga accattgcac atcaagagaa 840  
gaaaagtaat aaaaccaggt ttcatacaca gtccatggaa aagtgcatac atcagacagc 900  
acagaattga tactaactgg aggcgaggag aactcaaate tctaagggtg ctgaaaggac 960  
atgatgatca tgtgatcaca tgcttacagt tttgtggtaa ccgaatagtt agtggttctg 1020  
atgacaacac tttaaaagtt tggtcagcag tcacaggcaa atgtctgaga acattagtgg 1080

gacatacagg tggagtatgg tcatcacaaa tgagagacaa catcatcatt agtggatcta	1140
cagatcggac actcaaagtg tggaatgcag agactggaga atgtatacac accttatatg	1200
ggcatacttc cactgtgcgt tgtatgcac ttcatgaaaa aagagttgtt agcggttctc	1260
gagatgccac tcttaggggt tgggatattg agacaggcca gtgtttacat gttttgatgg	1320
gtcatgttgc agcagtcgcg tgtgttcaat atgatggcag gagggttgtt agtggagcat	1380
atgattttat ggtaaaggtg tgggatccag agactgaaac ctgtctacac acgttgcagg	1440
ggcatactaa tagagtctat tcattacagt ttgatggtat ccatgtggtg agtggatctc	1500
ttgatacatc aatccgtgtt tgggatgtgg agacaggga ttgcattcac acgttaacag	1560
ggcaccagtc gttaacaagt ggaatggaac tcaaagacaa tattcttgtc tctgggaatg	1620
cagattctac agttaaatac tgggatatca aaacaggaca gtgtttacaa acattgcaag	1680
gtcccaacaa gcatcagagt gctgtgacct gtttacagtt caacaagaac tttgtaatta	1740
ccagctcaga tgatggaact gtaaaactat gggacttgaa aacgggtgaa tttattcgaa	1800
acctagtcac attggagagt ggggggagtg ggggagttgt gtggcggatc agagcctcaa	1860
acacaaagct ggtgtgtgca gttgggagtc ggaatgggac tgaagaaacc aagctgctgg	1920
tgctggactt tgatgtggac atgaagtga gagcagaaaa gatgaatttg tccaattgtg	1980
tagacgatat actccctgcc cttccccctg caaaaagaaa aaaagaaaag aaaaagaaaa	2040
aaatcccttg ttctcagtg tgcaggatgt tggcttgggg caacagattg aaaagacctt	2100
cagactaaga aggaaaagaa gaagagatga caaaccataa ctgacaagag aggcgtctgc	2160
tgtctcatca cataaaaggc ttcacttttg actgagggca gctttgcaaa atgagacttt	2220
ctaaatcaaa ccaggtgcaa ttatttcttt attttcttct ccagtggcca ttggggcagt	2280
gttaatgctg aaacatcatt acagattctg ctagcctgtt cttttaccac tgacagctag	2340
acacctagaa aggaactgca ataatatcaa aacaagtact ggttgacttt ctaattagag	2400
agcatctgca acaaaaagtc atttttctgg agtggaaaag cttaaaaaaa ttactgtgaa	2460
ttgtttttgt acagttatca tgaaaagctt ttttttttat tttttngcca accattgcc	2520
atgtcaatca atcacagtat tagcctctgt taatctattt actgttgctt ccatatacat	2580
tcttcaatgc atatgttgct caaagggtggc aagttgtcct gggttctgtg agtcctgaga	2640
tggatttaat tcttgatgct ggtgctagaa gtaggtcttc aaatatggga ttgttgctcc	2700
aaccctgtac tgtactccca gtggccaaac ttatttatgc tgctaaatga aagaaagaaa	2760
aaagcaaatt atttttttta ttttttttct gctgtgacgt tttagtccca gactgaattc	2820

```

caaatttgc ttagtttggg tatggaaaaa agactttttg ccactgaaac ttgagccatc 2880
tgtgcctcta agaggctgag aatggaagag ttccagataa taaagagtga agtttgccctg 2940
caagtaaaga attgagagtg tgtgcaaagc ttattttctt ttatctgggc aaaaattaaa 3000
acacattcct tggaacagag ctattacttg cctgttctgt ggagaaactt ttctttttga 3060
gggctgtggg gaatggatga acgtacatcg taaaactgac aaaatatttt aaaaatatat 3120
aaaacacaaa attaaaataa agttgctggg cagtcttagt gttttacagt atttgggaaa 3180
acaactgtta cagttttatt gctctgagta actgacaaag cagaaactat tcagtttttg 3240
tagtaaaggc gtcacatgca aacaaacaaa atgaatgaaa cagtcaaagc gtttgccctca 3300
ttctccaaga gccacaactc aagctgaact gtgaaagtgg ttttaactg taccctaggc 3360
gatctttttt cctccttctg tttatttttt tgnttgtttt atttatagtc tgatttaaaa 3420
caatcagatt caagttgggt aatttttagt atgtaacaac ctgacatgat ggaggaaaac 3480
aacctttaaa gggattgtgt ctatgggttg attcacttag aaattttatt ttcttataac 3540
ttaagtgcaa taaaatgtgt tttttcatgt t 3571

```

<210> 3

<211> 627

<212> PRT

<213> Homo sapiens

<400> 3

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1

5

10

15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

20

25

30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

35

40

45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr

50

55

60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr

65

70

75

80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

85

90

95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu

100

105

110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr

115

120

125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg

130

135

140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met

145

150

155

160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu

165

170

175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile

180

185

190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu

195	200	205
Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala		
210	215	220
Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu		
225	230	235
Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile		
245	250	255
Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys		
260	265	270
Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly		
275	280	285
Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile		
290	295	300
Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp		
305	310	315
Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr		
325	330	335
Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn		
340	345	350



Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala

355

360

365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val

370

375

380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp

385

390

395

400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val

405

410

415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg

420

425

430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro

435

440

445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val

450

455

460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp

465

470

475

480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr

485

490

495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn

500	505	510
Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile		
515	520	525
Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln		
530	535	540
Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser		
545	550	555
Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe		
565	570	575
Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val		
580	585	590
Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser		
595	600	605
Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val		
610	615	620
Asp Met Lys		
625		

<210> 4

<211> 592

<212> PRT

<213> Homo sapiens

<400> 4

Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys Gly Leu Tyr

1

5

10

15

Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr Glu Ser Leu

20

25

30

Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr Leu Lys Met

35

40

45

Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg

50

55

60

Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser

65

70

75

80

Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp

85

90

95

Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser

100

105

110

Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser

115

120

125

Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser  
130 135 140

Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln  
145 150 155 160

Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr  
165 170 175

Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr  
180 185 190

Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu  
195 200 205

Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg  
210 215 220

Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr  
225 230 235 240

Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys  
245 250 255

Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu  
260 265 270

Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu

275	280	285
Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly		
290	295	300
His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile		
305	310	315 320
Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly		
325	330	335
Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met		
340	345	350
His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu		
355	360	365
Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly		
370	375	380
His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val		
385	390	395 400
Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu		
405	410	415
Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu		
420	425	430

Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile  
435 440 445

Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly  
450 455 460

His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val  
465 470 475 480

Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly  
485 490 495

Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val  
500 505 510

Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp  
515 520 525

Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn  
530 535 540

Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile  
545 550 555 560

Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly  
565 570 575

Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

580

585

590

&lt;210&gt; 5

&lt;211&gt; 553

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 5

Met Gly Phe Tyr Gly Thr Leu Lys Met Ile Phe Tyr Lys Met Lys Arg

1

5

10

15

Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu Gly Lys Lys

20

25

30

Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys

35

40

45

Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln

50

55

60

Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro Thr Gly Leu

65

70

75

80

Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu

85

90

95

Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr Gln Val Lys

100

105

110

His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser

115

120

125

Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro

130

135

140

Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu

145

150

155

160

Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile

165

170

175

Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys Pro Gly Phe

180

185

190

Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His Arg Ile Asp

195

200

205

Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val Leu Lys Gly

210

215

220

His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile

225

230

235

240



Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser Ala Val Thr

245

250

255

Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly Val Trp Ser

260

265

270

Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr

275

280

285

Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His Thr Leu Tyr

290

295

300

Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu Lys Arg Val

305

310

315

320

Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp Ile Glu Thr

325

330

335

Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala Val Arg Cys

340

345

350

Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr Asp Phe Met

355

360

365

Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His Thr Leu Gln

370

375

380

Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly Ile His Val

385

390

395

400

Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp Val Glu Thr

405

410

415

Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu Thr Ser Gly

420

425

430

Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala Asp Ser Thr

435

440

445

Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln

450

455

460

Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln Phe Asn Lys

465

470

475

480

Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys Leu Trp Asp

485

490

495

Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu Glu Ser Gly

500

505

510

Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu

515

520

525

Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu

530

535

540

Val Leu Asp Phe Asp Val Asp Met Lys

545

550

<210> 6

<211> 545

<212> PRT

<213> Homo sapiens

<400> 6

Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser Glu Val

1

5

10

15

Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr

20

25

30

Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly

35

40

45

Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr

50

55

60

Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln

65

70

75

80

Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp

85

90

95

Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro

100	105	110
Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu		
115	120	125
Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln		
130	135	140
Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg		
145	150	155
Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg		
165	170	175
Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala		
180	185	190
Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu		
195	200	205
Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys		
210	215	220
Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr		
225	230	235
Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val		
245	250	255

Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile

260

265

270

Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr

275

280

285

Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys

290

295

300

Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr

305

310

315

320

Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met

325

330

335

Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val

340

345

350

Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr

355

360

365

Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser

370

375

380

Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser

385

390

395

400

Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr

	405	410	415
Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu			
	420	425	430
Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr			
	435	440	445
Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala			
	450	455	460
Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp			
465	470	475	480
Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg			
	485	490	495
Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg			
	500	505	510
Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn			
	515	520	525
Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met			
	530	535	540
Lys			
545			

<210> 7

<211> 540

<212> PRT

<213> Homo sapiens

<400> 7

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu

1

5

10

15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu

20

25

30

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala

35

40

45

Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro

50

55

60

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro

65

70

75

80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr

85

90

95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp

100

105

110

Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe  
115 120 125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp  
130 135 140

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu  
145 150 155 160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys  
165 170 175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His  
180 185 190

Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val  
195 200 205

Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly  
210 215 220

Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser  
225 230 235 240

Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly  
245 250 255

Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr



260	265	270
Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His		
275	280	285
Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu		
290	295	300
Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp		
305	310	315
Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala		
325	330	335
Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr		
340	345	350
Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His		
355	360	365
Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly		
370	375	380
Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp		
385	390	395
Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu		
405	410	415

Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala

420

425

430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln

435

440

445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln

450

455

460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys

465

470

475

480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu

485

490

495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn

500

505

510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr

515

520

525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

530

535

540

<210> 8

<211> 589

<212> PRT

<213> Homo sapiens

<400> 8

Met Ser Lys Pro Gly Lys Pro Thr Leu Asn His Gly Leu Val Pro Val

1 5 10 15

Asp Leu Lys Ser Ala Lys Glu Pro Leu Pro His Gln Thr Val Met Lys

20 25 30

Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys Arg Arg

35 40 45

Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser

50 55 60

Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly

65 70 75 80

Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala

85 90 95

Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro

100 105 110

Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly

115 120 125

Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro

130 135 140

Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg

145 150 155 160

Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser

165 170 175

Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr

180 185 190

Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys

195 200 205

Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile

210 215 220

Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln

225 230 235 240

His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys

245 250 255

Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys

260 265 270

Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp

275 280 285

Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly

290

295

300

Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser

305

310

315

320

Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile

325

330

335

His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His

340

345

350

Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp

355

360

365

Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala

370

375

380

Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala

385

390

395

400

Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu

405

410

415

His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp

420

425

430

Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp

435

440

445

Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser

450

455

460

Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn

465

470

475

480

Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu

485

490

495

Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu

500

505

510

Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val

515

520

525

Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr

530

535

540

Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser

545

550

555

560

Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu

565

570

575

Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

580

585

<210> 9

<211> 559

<212> PRT

<213> Homo sapiens

<400> 9

Met Lys Ile Phe Ser Ile Ser Ile Ile Ala Gln Gly Leu Pro Phe Cys

1 5 10 15

Arg Arg Arg Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser

20 25 30

Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr

35 40 45

Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu

50 55 60

Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val

65 70 75 80

Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp

85 90 95

Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys

100 105 110

Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe

115	120	125	
Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val			
130	135	140	
Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys			
145	150	155	160
Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys			
	165	170	175
Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys			
	180	185	190
Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile			
	195	200	205
Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser			
	210	215	220
Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln			
	225	230	235
Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys			
	245	250	255
Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His			
	260	265	270



Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser

275

280

285

Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu

290

295

300

Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His

305

310

315

320

Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg

325

330

335

Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His

340

345

350

Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser

355

360

365

Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr

370

375

380

Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln

385

390

395

400

Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg

405

410

415

Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His

420	425	430	
Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser			
435	440	445	
Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln			
450	455	460	
Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr			
465	470	475	480
Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly			
485	490	495	
Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu			
500	505	510	
Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg			
515	520	525	
Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr			
530	535	540	
Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys			
545	550	555	

<210> 10

<211> 540

<212> PRT

<213> Homo sapiens

<400> 10

Met Lys Arg Lys Leu Asp His Gly Ser Glu Val Arg Ser Phe Ser Leu

1

5

10

15

Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr Thr Ser Thr Thr Gly Leu

20

25

30

Val Pro Cys Ser Ala Thr Pro Thr Thr Phe Gly Asp Leu Arg Ala Ala

35

40

45

Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile Thr Ser Val Gln Pro Pro

50

55

60

Thr Gly Leu Gln Glu Trp Leu Lys Met Phe Gln Ser Trp Ser Gly Pro

65

70

75

80

Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile Asp Ser Cys Glu Pro Thr

85

90

95

Gln Val Lys His Met Met Gln Val Ile Glu Pro Gln Phe Gln Arg Asp

100

105

110

Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala Leu Tyr Val Leu Ser Phe

115

120

125

Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala Gln Thr Cys Arg Tyr Trp

130

135

140

Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp Arg Glu Lys Cys Lys Glu

145

150

155

160

Glu Gly Ile Asp Glu Pro Leu His Ile Lys Arg Arg Lys Val Ile Lys

165

170

175

Pro Gly Phe Ile His Ser Pro Trp Lys Ser Ala Tyr Ile Arg Gln His

180

185

190

Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu Leu Lys Ser Pro Lys Val

195

200

205

Leu Lys Gly His Asp Asp His Val Ile Thr Cys Leu Gln Phe Cys Gly

210

215

220

Asn Arg Ile Val Ser Gly Ser Asp Asp Asn Thr Leu Lys Val Trp Ser

225

230

235

240

Ala Val Thr Gly Lys Cys Leu Arg Thr Leu Val Gly His Thr Gly Gly

245

250

255

Val Trp Ser Ser Gln Met Arg Asp Asn Ile Ile Ile Ser Gly Ser Thr

260

265

270

Asp Arg Thr Leu Lys Val Trp Asn Ala Glu Thr Gly Glu Cys Ile His

275	280	285
Thr Leu Tyr Gly His Thr Ser Thr Val Arg Cys Met His Leu His Glu		
290	295	300
Lys Arg Val Val Ser Gly Ser Arg Asp Ala Thr Leu Arg Val Trp Asp		
305	310	315 320
Ile Glu Thr Gly Gln Cys Leu His Val Leu Met Gly His Val Ala Ala		
325	330	335
Val Arg Cys Val Gln Tyr Asp Gly Arg Arg Val Val Ser Gly Ala Tyr		
340	345	350
Asp Phe Met Val Lys Val Trp Asp Pro Glu Thr Glu Thr Cys Leu His		
355	360	365
Thr Leu Gln Gly His Thr Asn Arg Val Tyr Ser Leu Gln Phe Asp Gly		
370	375	380
Ile His Val Val Ser Gly Ser Leu Asp Thr Ser Ile Arg Val Trp Asp		
385	390	395 400
Val Glu Thr Gly Asn Cys Ile His Thr Leu Thr Gly His Gln Ser Leu		
405	410	415
Thr Ser Gly Met Glu Leu Lys Asp Asn Ile Leu Val Ser Gly Asn Ala		
420	425	430

Asp Ser Thr Val Lys Ile Trp Asp Ile Lys Thr Gly Gln Cys Leu Gln

435

440

445

Thr Leu Gln Gly Pro Asn Lys His Gln Ser Ala Val Thr Cys Leu Gln

450

455

460

Phe Asn Lys Asn Phe Val Ile Thr Ser Ser Asp Asp Gly Thr Val Lys

465

470

475

480

Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile Arg Asn Leu Val Thr Leu

485

490

495

Glu Ser Gly Gly Ser Gly Gly Val Val Trp Arg Ile Arg Ala Ser Asn

500

505

510

Thr Lys Leu Val Cys Ala Val Gly Ser Arg Asn Gly Thr Glu Glu Thr

515

520

525

Lys Leu Leu Val Leu Asp Phe Asp Val Asp Met Lys

530

535

540

<210> 11

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 11

cgggatccac catggatgat ggatcgatga cacc

34

<210> 12

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 12

ggaattcctt aagggtatac agcatcaaag tcg

33

<210> 13

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 13

tcacttcatg tccacatcaa agtcc

25

<210> 14

<211> 26

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 14

ggtaattaca agttcttggt gaactg

26

<210> 15

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 15

ccctgcaacg tgtgtagaca gg

22

<210> 16

<211> 24

<212> DNA



<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 16

ccagtctctg cattccacac ttg

24

<210> 17

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 17

ctcagacagg tcaggacatt tgg

23

<210> 18

<211> 33

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 18

ggaattccat gaaaagattg gaccatgggt ctg

33

<210> 19

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 19

ggaattcctc acttcatgtc acatcaaagt ccag

34

<210> 20

<211> 1881

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged

homo sapiens

<400> 20

atggagcaaa agtcatttc tgaagaggac ttgaatgaaa tggagcaaaa gtcatttct 60  
gaagaggact tgaatgaaat ggagcaaaag ctcatcttg aagaggactt gaatgaaatg 120

gagcaaaagc tcatttctga agaggacttg aatgaaatgg agcaaaagct catttctgaa 180  
gaggacttga atgaaatgga gagcttgggc gacctcacca tggagcaaaa gctcatttct 240  
gaagaggact tgaattccat gaaaagaaag ttggaccatg gttctgaggt ccgctctttt 300  
tctttgggaa agaaaccatg caaagtctca gaatatacaa gtaccactgg gcttgtacca 360  
tggtcagcaa caccaacaac ttttggggac ctcagagcag ccaatggcca agggcaacaa 420  
cgacgccgaa ttacatctgt ccagccacct acaggcctcc aggaatggct aaaaatgttt 480  
cagagctgga gtggaccaga gaaattgctt gctttagatg aactcattga tagttgtgaa 540  
ccaacacaag taaaacatat gatgcaagtg atagaacccc agtttcaacg agacttcatt 600  
tcattgctcc ctaaagagtt ggcactctat gtgctttcat tcctggaacc caaagacctg 660  
ctacaagcag ctcagacatg tcgctactgg agaatttttg ctgaagacaa ctttctctgg 720  
agagagaaat gcaaagaaga ggggattgat gaaccattgc acatcaagag aagaaaagta 780  
ataaaaccag gtttcataca cagtccatgg aaaagtgcac acatcagaca gcacagaatt 840  
gatactaact ggaggcgagg agaactcaaa tctcctaagg tgctgaaagg acatgatgat 900  
catgtgatca catgcttaca gttttgtggt aaccgaatag ttagtggttc tgatgacaac 960  
actttaaaag tttggtcagc agtcacaggc aaatgtctga gaacattagt gggacatata 1020  
ggtggagtat ggtcatcaca aatgagggac aacatcatca ttagtggatc tacagatcgg 1080  
acactcaaag tgtggaatgc agagactgga gaatgtatac acaccttata tgggcatact 1140  
tccactgtgc gttgtatgca tcttcatgaa aaaagagttg ttagcgggtc tcgagatgcc 1200  
actcttaggg tttgggatat tgagacaggc cagtgtttac atgttttgat gggatcatgtt 1260  
gcagcagtcg gctgtgttca atatgatggc aggaggggtt ttagtggagc atatgatttt 1320  
atggtaaagg tgtgggatcc agagactgaa acctgtctac acacgttgca ggggcatact 1380  
aatagagtct attcattaca gtttgatggt atccatgtgg tgagtggatc tcttgataca 1440  
tccatccgtg tttgggatgt ggagacaggg aattgcattc acacgttaac agggcaccag 1500  
tcgttaacaa gtggaatgga actcaaagac aatattcttg tctctgggaa tgcagattct 1560  
acagttaaaa tctgggatat caaaacagga cagtgtttac aaacattgca aggtcccaac 1620  
aagcatcaga gtgctgtgac ctgtttacag ttcaacaaga actttgtaat taccagctca 1680  
gatgatggaa ctgtaaaact atgggacttg aaaacgggtg aatttattcg aaacctagtc 1740  
acattggaga gtggggggag tgggggagtt gtgtggcgga tcagagcctc aaacacaaaag 1800  
ctggtgtgtg cagttgggag tcggaatggg actgaagaaa ccaagctgct ggtgctggac 1860

tttgatgtgg acatgaagtg a

1881;

<210> 21

<211> 626

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: 6 myc tagged

homo sapien

<400> 21

Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln

1

5

10

15

Lys Leu Ile Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile

20

25

30

Ser Glu Glu Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu

35

40

45

Asp Leu Asn Glu Met Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn

50

55

60

Glu Met Glu Ser Leu Gly Asp Leu Thr Met Glu Gln Lys Leu Ile Ser

65

70

75

80

Glu Glu Asp Leu Asn Ser Met Lys Arg Lys Leu Asp His Gly Ser Glu

85

90

95

Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu Tyr

100

105

110

Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr Phe

115

120

125

Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg Ile

130

135

140

Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met Phe

145

150

155

160

Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu Ile

165

170

175

Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile Glu

180

185

190

Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu Ala

195

200

205

Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala Ala

210

215

220

Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu Trp

225

230

235

240

Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile Lys

245

250

255

Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys Ser

260

265

270

Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly Glu

275

280

285

Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile Thr

290

295

300

Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp Asn

305

310

315

320

Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr Leu

325

330

335

Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn Ile

340

345

350

Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala Glu

355

360

365

Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val Arg

370

375

380

Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp Ala

385	390	395	400
Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val Leu			
405	410	415	
Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg Arg			
420	425	430	
Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro Glu			
435	440	445	
Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val Tyr			
450	455	460	
Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp Thr			
465	470	475	480
Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr Leu			
485	490	495	
Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn Ile			
500	505	510	
Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile Lys			
515	520	525	
Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln Ser			
530	535	540	

Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser Ser

545

550

555

560

Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe Ile

565

570

575

Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val Trp

580

585

590

Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser Arg

595

600

605

Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val Asp

610

615

620

Met Lys

625

<210> 22

<211> 31

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer



<400> 22

gggtaccctt cattattccc tcgagttctt c

31

<210> 23

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 23

ggaattcctt catgtccaca tcaaagtcc

29

<210> 24

<211> 2010

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged

homo sapien

<400> 24

atgtgtgtcc cgagaagcgg ttgatactg agctgcattt gcctttactg tggagttttg 60

ttgccggttc tgctccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120

tctgtgacat acctacctga aaaaggttta tattgtcaga gactgccaaag cagccggaca 180

cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240

ttaaaaatga ttttttacia aatgaaaaga aagttggacc atggttctga ggtccgctct 300  
 ttttcttttg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360  
 ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420  
 caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480  
 tttcagagct ggagtgacc agagaaattg cttgcttttag atgaactcat tgatagttgt 540  
 gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600  
 atttcattgc tccctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660  
 ctgctacaag cagctcagac atgtcgctac tggagaatth tggctgaaga caaccttctc 720  
 tggagagaga aatgcaaaga agaggggatt gatgaacatc tgcacatcaa gagaagaaaa 780  
 gtaataaaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840  
 attgatacta actggaggcg aggagaactc aaatctccta aggtgctgaa aggacatgat 900  
 gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960  
 aacactttaa aagtttggtc agcagtcaca ggcaaagtgc tgagaacatt agtgggacat 1020  
 acaggtggag tatggtcatc acaaatgaga gacaacatca tcattagtgg atctacagat 1080  
 cggacactca aagtgtggaa tgcagagact ggagaatgta tacacacctt atatgggcat 1140  
 acttccactg tgcgttgtat gcacttctcat gaaaaaagag ttgttagcgg ttctcgagat 1200  
 gccactctta gggtttgga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260  
 gttgcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320  
 tttatggtaa aggtgtggga tccagagact gaaacctgtc tacacacgtt gcaggggcat 1380  
 actaatagag tctattcatt acagtttgat ggtatccatg tggtagtgg atctcttgat 1440  
 acatcaatcc gtgtttgga tgtggagaca gggaattgca ttcacacgtt aacagggcac 1500  
 cagtcgttaa caagtggaat ggaactcaaa gacaatatc ttgtctctgg gaatgcagat 1560  
 tctacagtta aaatctggga tatcaaaaca ggacagtgtt taaaacatt gcaaggtccc 1620  
 aacaagcatc agagtgtgtg gacctgttta cagttcaaca agaactttgt aattaccagc 1680  
 tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740  
 gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800  
 aagctggtgt gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctggtgctg 1860  
 gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920

tctagagggc ccttcgaagg taagcctatc cctaaccctc tctcgggtct cgattctacg 1980  
cgtaccgggtc atcatcacca tcaccattga 2010

<210> 25

<211> 669

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: V5HIS tagged

homo sapien

<400> 25

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1

5

10

15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

20

25

30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

35

40

45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr

50

55

60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr

65

70

75

80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

	85	90	95
Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu			
	100	105	110
Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr			
	115	120	125
Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg			
	130	135	140
Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met			
145	150	155	160
Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu			
	165	170	175
Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile			
	180	185	190
Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu			
	195	200	205
Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala			
	210	215	220
Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu			
225	230	235	240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile

245

250

255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys

260

265

270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly

275

280

285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile

290

295

300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp

305

310

315

320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr

325

330

335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn

340

345

350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala

355

360

365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val

370

375

380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp

385                      390                      395                      400

405                      410                      415

420

435                      440                      445

450                      455                      460

465                      470                      475                      480

485                      490                      495

500                      505                      510

515                      520                      525

530                      535                      540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser

545 550 555 560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe

565 570 575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val

580 585 590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser

595 600 605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val

610 615 620

Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu

625 630 635 640

Ser Arg Gly Pro Phe Glu Gly Lys Pro Ile Pro Asn Pro Leu Leu Gly

645 650 655

Leu Asp Ser Thr Arg Thr Gly His His His His His His

660 665

<210> 26

<211> 2001

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MYCHIS tagged

homo sapiens

<400> 26

```
atgtgtgtcc cgagaagcgg tttgatactg agctgcattt gcctttactg tggagttttg 60
ttgccgggttc tgetccctaa tcttcctttt ctgacgtgcc tgagcatgtc cacattagaa 120
tctgtgacat acctacctga aaaagggttta tattgtcaga gactgccaaag cagccggaca 180
cacgggggca cagaatcact gaaggggaaa aatacagaaa atatgggttt ctacggcaca 240
ttaaaaatga ttttttacia aatgaaaaga aagttggacc atggttctga ggtccgctct 300
ttttcttttg gaaagaaacc atgcaaagtc tcagaatata caagtaccac tgggcttgta 360
ccatgttcag caacaccaac aacttttggg gacctcagag cagccaatgg ccaagggcaa 420
caacgacgcc gaattacatc tgtccagcca cctacaggcc tccaggaatg gctaaaaatg 480
tttcagagct ggagtggacc agagaaattg cttgctttag atgaactcat tgatagttgt 540
gaaccaacac aagtaaaaca tatgatgcaa gtgatagaac cccagtttca acgagacttc 600
atttcattgc tccctaaaga gttggcactc tatgtgcttt cattcctgga acccaaagac 660
ctgctacaag cagctcagac atgtcgctac tggagaattt tggctgaaga caaccttctc 720
tggagagaga aatgcaaaga agaggggatt gatgaaccat tgcacatcaa gagaagaaaa 780
gtaataaaac caggtttcat acacagtcca tggaaaagtg catacatcag acagcacaga 840
attgatacta actggaggcg aggagaactc aaatctccta aggtgctgaa aggacatgat 900
gatcatgtga tcacatgctt acagttttgt ggtaaccgaa tagttagtgg ttctgatgac 960
aacactttaa aagtttggtc agcagtcaca ggcaaatgtc tgagaacatt agtgggacat 1020
acaggtggag tatggtcac cacaatgaga gacaacatca tcattagtgg atctacagat 1080
cggacactca aagtgtggaa tgcagagact ggagaatgta tacacacctt atatgggcat 1140
acttccactg tgcgttgtat gcattctcat gaaaaaagag ttgttagcgg ttctcgagat 1200
gccactctta gggtttggga tattgagaca ggccagtgtt tacatgtttt gatgggtcat 1260
```



gttgcagcag tccgctgtgt tcaatatgat ggcaggaggg ttgttagtgg agcatatgat 1320  
 tttatggtaa aggtgtggga tccagagact gaaacctgtc tacacacggt gcaggggcat 1380  
 actaatagag tctattcatt acagtttgat ggtatccatg tggtagagtgg atctcttgat 1440  
 acatcaatcc gtgtttggga tgtggagaca gggaattgca ttcacacggt aacagggcac 1500  
 cagtcgtaa caagtggaat ggaactcaaa gacaatatc ttgtctctgg gaatgcagat 1560  
 tctacagtta aaatctggga tatcaaaaca ggacagtgtt taaaacatt gcaaggtccc 1620  
 aacaagcatc agagtgtgtg gacctgttta cagttcaaca agaactttgt aattaccagc 1680  
 tcagatgatg gaactgtaaa actatgggac ttgaaaacgg gtgaatttat tcgaaaccta 1740  
 gtcacattgg agagtggggg gagtggggga gttgtgtggc ggatcagagc ctcaaacaca 1800  
 aagctggtgt gtgcagttgg gagtcggaat gggactgaag aaaccaagct gctggtgctg 1860  
 gactttgatg tggacatgaa ggaattctgc agatatccag cacagtggcg gccgctcgag 1920  
 tctagagggc ccttcgaaca aaaactcatc tcagaagagg atctgaatat gcataccggt 1980  
 catcatcacc atcaccattg a 2001

<210> 27

<211> 666

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: MYCHIS tagged

homo sapiens

<400> 27

Met Cys Val Pro Arg Ser Gly Leu Ile Leu Ser Cys Ile Cys Leu Tyr

1

5

10

15

Cys Gly Val Leu Leu Pro Val Leu Leu Pro Asn Leu Pro Phe Leu Thr

20

25

30

Cys Leu Ser Met Ser Thr Leu Glu Ser Val Thr Tyr Leu Pro Glu Lys

35

40

45

Gly Leu Tyr Cys Gln Arg Leu Pro Ser Ser Arg Thr His Gly Gly Thr

50

55

60

Glu Ser Leu Lys Gly Lys Asn Thr Glu Asn Met Gly Phe Tyr Gly Thr

65

70

75

80

Leu Lys Met Ile Phe Tyr Lys Met Lys Arg Lys Leu Asp His Gly Ser

85

90

95

Glu Val Arg Ser Phe Ser Leu Gly Lys Lys Pro Cys Lys Val Ser Glu

100

105

110

Tyr Thr Ser Thr Thr Gly Leu Val Pro Cys Ser Ala Thr Pro Thr Thr

115

120

125

Phe Gly Asp Leu Arg Ala Ala Asn Gly Gln Gly Gln Gln Arg Arg Arg

130

135

140

Ile Thr Ser Val Gln Pro Pro Thr Gly Leu Gln Glu Trp Leu Lys Met

145

150

155

160

Phe Gln Ser Trp Ser Gly Pro Glu Lys Leu Leu Ala Leu Asp Glu Leu

165

170

175

Ile Asp Ser Cys Glu Pro Thr Gln Val Lys His Met Met Gln Val Ile

180

185

190

Glu Pro Gln Phe Gln Arg Asp Phe Ile Ser Leu Leu Pro Lys Glu Leu

195

200

205

Ala Leu Tyr Val Leu Ser Phe Leu Glu Pro Lys Asp Leu Leu Gln Ala

210

215

220

Ala Gln Thr Cys Arg Tyr Trp Arg Ile Leu Ala Glu Asp Asn Leu Leu

225

230

235

240

Trp Arg Glu Lys Cys Lys Glu Glu Gly Ile Asp Glu Pro Leu His Ile

245

250

255

Lys Arg Arg Lys Val Ile Lys Pro Gly Phe Ile His Ser Pro Trp Lys

260

265

270

Ser Ala Tyr Ile Arg Gln His Arg Ile Asp Thr Asn Trp Arg Arg Gly

275

280

285

Glu Leu Lys Ser Pro Lys Val Leu Lys Gly His Asp Asp His Val Ile

290

295

300

Thr Cys Leu Gln Phe Cys Gly Asn Arg Ile Val Ser Gly Ser Asp Asp

305

310

315

320

Asn Thr Leu Lys Val Trp Ser Ala Val Thr Gly Lys Cys Leu Arg Thr

325

330

335

Leu Val Gly His Thr Gly Gly Val Trp Ser Ser Gln Met Arg Asp Asn

340

345

350

Ile Ile Ile Ser Gly Ser Thr Asp Arg Thr Leu Lys Val Trp Asn Ala

355

360

365

Glu Thr Gly Glu Cys Ile His Thr Leu Tyr Gly His Thr Ser Thr Val

370

375

380

Arg Cys Met His Leu His Glu Lys Arg Val Val Ser Gly Ser Arg Asp

385

390

395

400

Ala Thr Leu Arg Val Trp Asp Ile Glu Thr Gly Gln Cys Leu His Val

405

410

415

Leu Met Gly His Val Ala Ala Val Arg Cys Val Gln Tyr Asp Gly Arg

420

425

430

Arg Val Val Ser Gly Ala Tyr Asp Phe Met Val Lys Val Trp Asp Pro

435

440

445

Glu Thr Glu Thr Cys Leu His Thr Leu Gln Gly His Thr Asn Arg Val

450

455

460

Tyr Ser Leu Gln Phe Asp Gly Ile His Val Val Ser Gly Ser Leu Asp

465

470

475

480

Thr Ser Ile Arg Val Trp Asp Val Glu Thr Gly Asn Cys Ile His Thr

485

490

495

Leu Thr Gly His Gln Ser Leu Thr Ser Gly Met Glu Leu Lys Asp Asn

500

505

510

Ile Leu Val Ser Gly Asn Ala Asp Ser Thr Val Lys Ile Trp Asp Ile

515

520

525

Lys Thr Gly Gln Cys Leu Gln Thr Leu Gln Gly Pro Asn Lys His Gln

530

535

540

Ser Ala Val Thr Cys Leu Gln Phe Asn Lys Asn Phe Val Ile Thr Ser

545

550

555

560

Ser Asp Asp Gly Thr Val Lys Leu Trp Asp Leu Lys Thr Gly Glu Phe

565

570

575

Ile Arg Asn Leu Val Thr Leu Glu Ser Gly Gly Ser Gly Gly Val Val

580

585

590

Trp Arg Ile Arg Ala Ser Asn Thr Lys Leu Val Cys Ala Val Gly Ser

595

600

605

Arg Asn Gly Thr Glu Glu Thr Lys Leu Leu Val Leu Asp Phe Asp Val

610

615

620

Asp Met Lys Glu Phe Cys Arg Tyr Pro Ala Gln Trp Arg Pro Leu Glu

625

630

635

640

Ser Arg Gly Pro Phe Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu Asn

645

650

655

Met His Thr Gly His His His His His His

660

665

<210> 28

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 28

tcacttcatgtccacatcaaagtc

25

<210> 29

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 29

ggtaattacaaagttcttggtgaactg

27

<210> 30

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 30

ccctgcaacgtgtgtagacagg

22

<210> 31

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 31

ccagtctctgcattccacactttg

24

<210> 32

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:

Oligonucleotide primer

<400> 32

ctcagacaggtcaggacatttgg

23